

Db		236	GCTTCCTTCTGACAGCAGAGGTCGACTTATCAAGGATCTCCCTCACTGGACACAG	295
Qy		81	LeuLysAlaAspGluLysTyrPheIleSerHisIleLeuAlaPhePheAlaAlaSerAsp	100
Db		296	CTTAAAGCAGATGAGAGTACTTCTCATCTTAGCCCTTTTTCAGCCAGTGAT	355
Qy		101	GlyIleValAsnGluAsnLeuValGluArgPheSerGlnGluValGlnValProGluAla	120
Db		356	GGAAATGTAAATGAAATTTGGTGGAGCCCTTTAGTCAGAGGTCGAGGTCACAGGCT	415
Qy		121	ArgCysPheTyrGlyPheGlnIleLeuIleGluAsnValHisSerGluMetTyrSerLeu	140
Db		416	CGCTGTTCTATGGCTTTCAAAATCTCATCGAATGTTCACTCAGAGATGTACAGTTTG	475
Qy		141	LeuIleAspThrTyrIleArgAspProLysLysArgGluPheLeuPheAsnAlaIleGlu	160
Db		476	CTGATAGACACTTACATCAGAGATCCCAAGAAAGGGAATTTTATTTAATGCAATTGAA	535
Qy		161	ThrMetProTyrValLysLysLysAlaAspTdpAlaLeuArgTTrIleAlaAspArgLys	180
Db		536	ACCATGCCCTATGTAAAGAAAGCAGATGGGCCCTTGCATGATAGATAGATAGAAAA	595
Qy		181	SerThrPheGlyGluArgValValAlaPheAlaAlaValGluGlyValPhePheSerGly	200
Db		596	TCTACTTTTGGGGAAGAGTGGTGGCTTTGCTGTGTAGAGGAGTTTCTTCTCAGGA	655
Qy		201	SerPheAlaAlaIlePheTrpLeuLysLysArgGlyLeuMetProGlyLeuThrPheSer	220
Db		656	TCCTTTTGCTGCTATATTGCTTAAAGAGAGAGGTCCTTATGCCAGGACTCACTTTTCC	715
Qy		221	AsnGluLeuIleSerArgAspGluGlyLeuHisCysAspPheAlaCysLeuMetPheGln	240
Db		716	AATGAACCTCATCAGCAGAGATGAAGGACTTCACTGTGACTTTGCTTGCCTGATGTTCAA	775
Qy		241	TyrLeuValAsnLysProSerGluArgValArgGluIleIleValAspAlaValLys	260
Db		776	TACTTAGTAAATAGCCCTTCAAGAAAGGGTCAGGAGATCATTTGTGATGCTGTCAAA	835
Qy		261	IleGluGlnGluPheLeuThrGluAlaLeuProValGlyLeuIleGlyMetAsnCysIle	280
Db		836	ATTGAGCAGGAGTTTAAACAGAGCCCTTGCCAGTTGGCTCATTTGGAATGAATTGCATT	895
Qy		281	LeuMetLysGlnTyrIleGluPheValAlaAspArgLeuLeuValGluLeuGlyPheSer	300
Db		896	TTGATCAAAACAGTACATTGAGTTTGTAGCTGACAGATTACTTTGTGGAACTTGGATTCTCA	955
Qy		301	LysValPheGlnAlaGluAsnProPheAspPheMetGluAsnIleSerLeuGluGlyLys	320
Db		956	AAGGTTTTTTCAGGCAGAAATCCTTTTGATTTTATGGAACACATTTCTTTAGAGGAAAA	1015
Qy		321	ThrAsnPhePheGluLysArgValSerGluTyrGlnArgPheAlaValMetAlaGluThr	340
Db		1016	ACAAATTTCTTTGAGAAACAGTTTCAGAGTATCAGCGTTTTCAGTTATGGCAGAAACC	1075
Qy		341	ThrAspAsnValPheThrLeuAspAlaAspPhe	351
Db		1076	ACAGATAAGCTCTTCACTTGGATGCAGATTTT	1108

RESULT 5
 AAF32439
 ID AAF32439 standard; cDNA; 4955 BP.
 XX
 AC AAF32439;
 XX
 DT 18-APR-2001 (first entry)
 XX
 DE Human ribonucleotide reductase related nucleotide sequence SEQ ID NO:3.
 XX
 KW Human; ribonucleotide reductase; cancer; DNA repair; p53; ss.
 XX
 OS Homo sapiens.
 XX

Db 836 95
 QY 281 00
 Db 896 35
 QY 301 20
 Db 956 115
 QY 321 0
 Db 1016 175
 QY 341
 Db 1076

RESULT 5

US-60-128-660-20
 ; Sequence 20, Application US/60128660
 ; GENERAL INFORMATION:
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Yue, Henry
 ; APPLICANT: Yang, Junming
 ; APPLICANT: Baughn, Mariah R.
 ; FILE OF INVENTION: RNA-ASSOCIATED PROTEINS
 ; FILE REFERENCE: PF-0682 P
 ; CURRENT APPLICATION NUMBER: US/60/128,660
 ; CURRENT FILING DATE: 1999-04-08
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 20
 ; LENGTH: 2596
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: 2604449
 US-60-128-660-20

Alignment Scores:

Pred. No.: 1.3e-193 Length: 2596
 Score: 1821.00 Matches: 351
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 81 Gaps: 0

US-10-698-228-1 (1-351) x US-60-128-660-20 (1-2596)

QY 1 MetGlyAspProGluArgProGluAlaAlaGlyLeuAspGlnAspGluArgSerSer 20
 Db 56 ATGGCGCACCGCGGAAAGCGCGCGGCTGGATCAGGATCAGGATCATCTTCA 115
 QY 21 AspThrAsnGluSerGluLeuLysSerAsnGluProLeuLeuArgLysSerArg 40
 Db 116 GACACCAACGAAAGTGAATATAGTCAATGAGAGGCCACTCTTAAGAAAGTTCTCGC 175
 QY 41 ArgPheValIlePheProIleGlnTyrProAspIleTrpLysMetTyrLysGlnAlaGln 60
 Db 176 CGGTTTGTCATCTTTCCATCCAGTACCTGATATTGGAAAAATGTATAAACAGGCACAG 235
 QY 61 AlaserPheTrpThrAlaGluGluValAspLeuSerLysAspLeuProHisTrpAsnLys 80
 Db 236 GCTTCCTCTCGGACAGCAGAGAGGTGCGACTTATCAAGAGGATCTCCCTCACTGGAAACAAG 295
 QY 81 LeuLysAlaAspGluLysTyrPheIleSerHisIleLeuAlaPheAlaAlaSerAsp 100
 Db 296 CTTAAGCAGATGAGAGTACTTCTCATCTCTCAGCTTTTGTGAGCCAGTGAT 355

David M. M. M.

HUMA
OF



Db 56 ATGGCGGACCGGAAAGCGGCGGCTGGATCAGATGAGAGATCATCTTCA 115
Qy 61 GACACCAACGAAGTGAATAAAGTCAATGAAGAGCCCTCTTAAGAAAGAGTTCTCGC 120
Db 116 GACACCAACGAAGTGAATAAAGTCAATGAAGAGCCCTCTTAAGAAAGAGTTCTCGC 175
Qy 121 CGGTTTGTCTATCTTCCATCCAGTACCTCTGATATTTGGAAATGTATAAACAGGCACAG 180
Db 176 CGGTTTGTCTATCTTCCATCCAGTACCTCTGATATTTGGAAATGTATAAACAGGCACAG 235
Qy 181 GCTTCCTCTCTGACAGCAGAGAGGTGAGCTTATCAAGGATCTCCCTCACTGGAAACAAG 240
Db 236 GCTTCCTCTCTGACAGCAGAGAGGTGAGCTTATCAAGGATCTCCCTCACTGGAAACAAG 295
Qy 241 CTTAAAGCAGATGAGAGATCTTCAATCTCTCAATCTTAGCCCTTTTTCAGCCAGTGAT 300
Db 296 CTTAAAGCAGATGAGAGATCTTCAATCTCTCAATCTTAGCCCTTTTTCAGCCAGTGAT 355
Qy 301 GGAATTTGAATGAATAAATTTGGTGGAGCGCTTTAGTCAGAGGTGCGAGTTCCAGAGGCT 360
Db 356 GGAATTTGAATGAATAAATTTGGTGGAGCGCTTTAGTCAGAGGTGCGAGTTCCAGAGGCT 415
Qy 361 CGCTGTTCTATGCGCTTTCAAATTTCTCATCGAATGTTCACTCAGAGATGTACAGTTTG 420
Db 416 CGCTGTTCTATGCGCTTTCAAATTTCTCATCGAATGTTCACTCAGAGATGTACAGTTTG 475
Qy 421 CTGATAGACACTTACATCAGAGATCCCAAGAAAGGAATTTTATTAATGAATGAA 480
Db 476 CTGATAGACACTTACATCAGAGATCCCAAGAAAGGAATTTTATTAATGAATGAA 535
Qy 481 ACCATGCCCTATGTTAAGAAAGAGAGTGGCGCTTGGCTAGAGAGGATTTTCTTCTCAGGA 540
Db 536 ACCATGCCCTATGTTAAGAAAGAGAGTGGCGCTTGGCTAGAGAGGATTTTCTTCTCAGGA 595
Qy 541 TCTACTTTTGGGAAAGAGTGGCGCTTGGCTAGAGAGGATTTTCTTCTCAGGA 600
Db 596 TCTACTTTTGGGAAAGAGTGGCGCTTGGCTAGAGAGGATTTTCTTCTCAGGA 655
Qy 601 TCTTTTGTCTATATTTCTGGCTAAAGAGAGGATTTATGCGAGAGTCACTTTTTC 660
Db 656 TCTTTTGTCTATATTTCTGGCTAAAGAGAGGATTTATGCGAGAGTCACTTTTTC 715
Qy 661 AATGAACCTCATCAGCAGAGATGAAGACTTCACTGTGACTTGGCTGCTGATGTTCCAA 720
Db 716 AATGAACCTCATCAGCAGAGATGAAGACTTCACTGTGACTTGGCTGCTGATGTTCCAA 775
Qy 721 TACTTAGTAATTAAGCCTTCAGAAAGAGGATCAGGAGATCATTTGATGCTGTCAA 780
Db 776 TACTTAGTAATTAAGCCTTCAGAAAGAGGATCAGGAGATCATTTGATGCTGTCAA 835
Qy 781 ATTGAGCAGAGATTTTAAACAGAGCCCTTGCAGTGGCCCTCATTTGGAATGAATGCATT 840
Db 836 ATTGAGCAGAGATTTTAAACAGAGCCCTTGCAGTGGCCCTCATTTGGAATGAATGCATT 895
Qy 841 TTGATGAACAGTACATTGAGTTTGTAGCTGACAGATTACTTGTGGAACTTGGATTCTCA 900
Db 896 TTGATGAACAGTACATTGAGTTTGTAGCTGACAGATTACTTGTGGAACTTGGATTCTCA 955
Qy 901 AAGGTTTTTTCAGGCAGAAATCCTTTTGAATTTATGGAATAACATTTCTTTAGAGGAAAA 960
Db 956 AAGGTTTTTTCAGGCAGAAATCCTTTTGAATTTATGGAATAACATTTCTTTAGAGGAAAA 1015
Qy 961 ACAATTTCTTTGAGAAACGAGTTTTCAGAGTATCAGCGTTTTCAGATTATGGCAGAAACC 1020
Db 1016 ACAATTTCTTTGAGAAACGAGTTTTCAGAGTATCAGCGTTTTCAGATTATGGCAGAAACC 1075
Qy 1021 ACAGATAACGTTCTCACCTTGGATGCAGATTTT 1053
Db 1076 ACAGATAACGTTCTCACCTTGGATGCAGATTTT 1108

Sequence 20, Application US/60128660
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Yang, Junming
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: RNA-ASSOCIATED PROTEINS
FILE REFERENCE: PP-0682 P
CURRENT APPLICATION NUMBER: US/60/128,660
CURRENT FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PERL Program
SEQ ID NO 20
LENGTH: 2596
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: 2604449
US-60-128-660-20

Query Match 100.0%; Score 1053; DB 81; Length 2596;
Best Local Similarity 100.0%; Pred. No. 2.9e-276;
Matches 1053; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGACCGCGAAGCGCGCGGCTGGATCAGATGAGAGATCATCTTCA 60
DB |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 56 ATGGCGGACCGCGAAGCGCGCGGCTGGATCAGATGAGAGATCATCTTCA 115
DB |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 61 GACACCAACGAAAGTGAATAAGTCAATGAAGAGCCACTCTTAAGAAAGATTCTCGC 120
DB |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 116 GACACCAACGAAAGTGAATAAGTCAATGAAGAGCCACTCTTAAGAAAGATTCTCGC 175
DB |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 121 CGTTTGTGCACTTTCCAAATCAGTACCTGATATTTGAAAATGTATTAACAGGCACAG 180
DB |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 176 CGTTTGTGCACTTTCCAAATCAGTACCTGATATTTGAAAATGTATTAACAGGCACAG 235
DB |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 181 GCTTCTCTGACGACGAGAGGTCGATCTCAAGAGATCTCCCTCAGTGAACACAG 240
DB |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 236 GCTTCTCTGACGACGAGAGGTCGATCTCAAGAGATCTCCCTCAGTGAACACAG 295
DB |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 241 CTTAAGCAGATGAGAAGTACTTCTCATCTCTAGCCCTTTTTCAGCCAGTGAT 300
DB |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 296 CTTAAGCAGATGAGAAGTACTTCTCATCTCTAGCCCTTTTTCAGCCAGTGAT 355
DB |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 301 GGAATTGTAATGAAAATTTGTGGAGCGCTTTAGTCAGAGGTGCGAGTTCAGAGGCT 360
DB |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 356 GGAATTGTAATGAAAATTTGTGGAGCGCTTTAGTCAGAGGTGCGAGTTCAGAGGCT 415
DB |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 361 CGCTGTTCTATGGCTTTTCAAAATCTCATCGAGATGTTCACTCAGAGATGTACAGTTTG 420
DB |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 416 CGCTGTTCTATGGCTTTTCAAAATCTCATCGAGATGTTCACTCAGAGATGTACAGTTTG 475
DB |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 421 CTGATAGACACTTACATCAGAGATCCCAAGAAAGGGAATTTTATTAATGCAATTGAA 480
DB |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 476 CTGATAGACACTTACATCAGAGATCCCAAGAAAGGGAATTTTATTAATGCAATTGAA 535
DB |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 481 ACCATGCCCTATGTTAAGAAAAGCAGATGCGGCTTGGATGGATAGCAGATAGAAA 540
DB |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 536 ACCATGCCCTATGTTAAGAAAAGCAGATGCGGCTTGGATGGATAGCAGATAGAAA 595
DB |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 541 TCTACTTTTGGGAAAGAGTGGGCTTTGCTGCTGATAGAGGAGTTTCTTCTCAGGA 600
DB |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 596 TCTACTTTTGGGAAAGAGTGGGCTTTGCTGCTGATAGAGGAGTTTCTTCTCAGGA 655
DB |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 601 TCTTTTGTGCTATATTTCTGGCTAAAGAGAGAGGCTTTATGCCAGGACTCACTTTTTC 660
DB |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 656 TCTTTTGTGCTATATTTCTGGCTAAAGAGAGAGGCTTTATGCCAGGACTCACTTTTTC 715
DB |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 661 AATGAATCATCAGCAGATGAGGACTTCACTGTGACTTTGCTTGTGCTGTGATGTTCCAA 720
DB |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 716 AATGAATCATCAGCAGATGAGGACTTCACTGTGACTTTGCTTGTGCTGTGATGTTCCAA 775
DB |||||||||||||||||||||||||||||||||||||||||||||||||||

non-biased

QY 721 TACTTAGTAAATAAGCCCTTCAGAAAGAAAGGCTCAGGGAGATCATTTGTTGATGCTCTCAAA 780
DB |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 776 TACTTAGTAAATAAGCCCTTCAGAAAGAAAGGCTCAGGGAGATCATTTGTTGATGCTCTCAAA 835
DB |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 781 ATTGAGCAGGAGTTTAAACAGAACCTTCCAGTTCGCTCATTTGGAAATGAATTCATT 840
DB |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 836 ATTGAGCAGGAGTTTAAACAGAACCTTCCAGTTCGCTCATTTGGAAATGAATTCATT 895
DB |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 841 TTGATGAAACAGTACATTGAGTTTGTAGCTGACAGATTACTTGTGAACTTTGGATTCTCA 900
DB |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 896 TTGATGAAACAGTACATTGAGTTTGTAGCTGACAGATTACTTGTGAACTTTGGATTCTCA 955
DB |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 901 AAGGTTTTTCAGGCGAGAAAATCCTTTTGAATTTTATGAAAAACATTTCTTTAGAGGAAA 960
DB |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 956 AAGGTTTTTCAGGCGAGAAAATCCTTTTGAATTTTATGAAAAACATTTCTTTAGAGGAAA 1015
DB |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 961 ACAAATTTCTTTGAGAAACGAGTTTCAGAGTATCAGCGTTTTCAGAGTTATGTCAGAAACC 1020
DB |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1016 ACAAATTTCTTTGAGAAACGAGTTTCAGAGTATCAGCGTTTTCAGAGTTATGTCAGAAACC 1075
DB |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1021 ACAGATAACGCTTTCACCTTGGATGACAGATTTT 1053
DB |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1076 ACAGATAACGCTTTCACCTTGGATGACAGATTTT 1108
DB |||||||||||||||||||||||||||||||||||||||||||||||||||